Response to Office Action of March 26, 2003
Application No. 09/888,264

IN THE SPECIFICATION

Please amend the paragraph on page 6, lines 3-22 as follows:

"Percent (%) amino acid sequence identity" with respect to the human OGC sequences identified herein is defined as the percentage of amino acid residues in human OGC sequence that are identical with the amino acid residues in the candidate sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. % identity can be determined by WU-BLAST-2, obtained from (Altschul e~al., 1996. Methods in Enzymology, 266: 460-480); http://blast.wustl/edu/blast/READ ME.html. WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched; however, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).